OIPE

RAW SEQUENCE LISTING   DATE: 08/13/2001
PATENT APPLICATION: US/09/922,488   TIME: 11:25:00

Input Set : A:\0054.txt
Output Set: N:\CRF3\08132001\I922488.raw

ENTERED

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        4 <110> APPLICANT: Thayer, Edward C.
        5        Webster, Philippa J.
        7 <120> TITLE OF INVENTION: Human Secreted Protein, Zzp1
        9 <130> FILE REFERENCE: 00-54
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/922,488
C--> 11 <141> CURRENT FILING DATE: 2001-08-03
       11 <150> PRIOR APPLICATION NUMBER: 60/222,814
       12 <151> PRIOR FILING DATE: 2000-08-04
       14 <150> PRIOR APPLICATION NUMBER: 60/260,512
       15 <151> PRIOR FILING DATE: 2001-01-09
       17 <160> NUMBER OF SEQ ID NOS: 5
       19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
       21 <210> SEQ ID NO: 1
       22 <211> LENGTH: 1908
       23 <212> TYPE: DNA
       24 <213> ORGANISM: Homo sapiens
       26 <220> FEATURE:
       27 <221> NAME/KEY: CDS
       28 <222> LOCATION: (1)...(1908)
       30 <400> SEQUENCE: 1
       31 atg gca gga ggc tca gcc acg acc tgg ggt tac cct gtg gcc ctg cta   48
       32 Met Ala Gly Gly Ser Ala Thr Thr Trp Gly Tyr Pro Val Ala Leu Leu
       33 1               5                  10                  15
       35 ctg ctg gtt gcc acc ctg ggg ctg ggt agg tgg ctc cag ccc gac cca   96
       36 Leu Leu Val Ala Thr Leu Gly Leu Gly Arg Trp Leu Gln Pro Asp Pro
       37              20                  25                  30
       39 ggc ctc cgg cac agc tac gac tgt ggg atc aag gga atg cag ctg ctg   144
       40 Gly Leu Arg His Ser Tyr Asp Cys Gly Ile Lys Gly Met Gln Leu Leu
       41          35                  40                  45
       44 gtg ttc ccc agg cca ggc cag act ctc cgc ttc aag gtg gtg gat gaa   192
       45 Val Phe Pro Arg Pro Gly Gln Thr Leu Arg Phe Lys Val Val Asp Glu
       46      50                  55                  60
       48 ttt ggg aac cga ttt gat gtc aac aac tgc tcc atc tgc tac cac tgg   240
       49 Phe Gly Asn Arg Phe Asp Val Asn Asn Cys Ser Ile Cys Tyr His Trp
       50 65                  70                  75                  80
       52 gtc acc tcc agg ccg cag gag cct gca gtc ttc tcg gcc gat tac aga   288
       53 Val Thr Ser Arg Pro Gln Glu Pro Ala Val Phe Ser Ala Asp Tyr Arg
       54                  85                  90                  95
       56 ggc tgc cac gtg ctg gag aag gat ggg cgt ttc cac ctg agg gtg ttc   336
       57 Gly Cys His Val Leu Glu Lys Asp Gly Arg Phe His Leu Arg Val Phe
       58              100                 105                 110
       60 atg gag gct gtg ctg ccc aat ggt cgt gtg gat gtg gca caa gac gct   384
       61 Met Glu Ala Val Leu Pro Asn Gly Arg Val Asp Val Ala Gln Asp Ala
       62              115                 120                 125
       64 act ctg atc tgt ccc aaa cct gac ccc tcc cgg act ctg gac tcc cag   432
       65 Thr Leu Ile Cys Pro Lys Pro Asp Pro Ser Arg Thr Leu Asp Ser Gln
       66          130                 135                 140
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 68 ctg gca cca ccc gcc atg ttc tct gtc tca acc cca caa acc ctt tcc    480
 69 Leu Ala Pro Pro Ala Met Phe Ser Val Ser Thr Pro Gln Thr Leu Ser
 70 145                 150                 155                 160
 72 ttc ctc ccc acc tct ggc cat acc tcc caa ggc tct ggc cat gcc ttt    528
 73 Phe Leu Pro Thr Ser Gly His Thr Ser Gln Gly Ser Gly His Ala Phe
 74                 165                 170                 175
 76 ccc agc cca ctg gac cca ggg cac agc tct gtc cac cca acc cct gct    576
 77 Pro Ser Pro Leu Asp Pro Gly His Ser Ser Val His Pro Thr Pro Ala
 78                 180                 185                 190
 80 tta cca tcc cct gga cct gga cct acc ctc gcc acc ctg gct caa ccc    624
 81 Leu Pro Ser Pro Gly Pro Gly Pro Thr Leu Ala Thr Leu Ala Gln Pro
 82             195                 200                 205
 84 cac tgg ggc acc ttg gaa cac tgg gat gtg aac aaa cga gat tac ata    672
 85 His Trp Gly Thr Leu Glu His Trp Asp Val Asn Lys Arg Asp Tyr Ile
 86     210                 215                 220
 88 ggt acc cac ctg agc cag gag cag tgc cag gtg gcc tca ggg cac ctc    720
 89 Gly Thr His Leu Ser Gln Glu Gln Cys Gln Val Ala Ser Gly His Leu
 90 225                 230                 235                 240
 92 ccc tgc atc gtg aga aga act tca aaa gaa gcc tgt cag cag gct ggc    768
 93 Pro Cys Ile Val Arg Arg Thr Ser Lys Glu Ala Cys Gln Gln Ala Gly
 94                 245                 250                 255
 96 tgc tgc tat gac aac acc aga gag gtt ccc tgt tac tat ggc aac aca    816
 97 Cys Cys Tyr Asp Asn Thr Arg Glu Val Pro Cys Tyr Tyr Gly Asn Thr
 98                 260                 265                 270
100 gct act gtc cag tgc ttc aga gat ggc tac ttc gtc ctc gta gtg tcc    864
101 Ala Thr Val Gln Cys Phe Arg Asp Gly Tyr Phe Val Leu Val Val Ser
102             275                 280                 285
104 caa gaa atg gcc ttg aca cac agg atc aca ctg gcc aac atc cac ctg    912
105 Gln Glu Met Ala Leu Thr His Arg Ile Thr Leu Ala Asn Ile His Leu
106         290                 295                 300
108 gcc tat gcc ccc acc agc tgc tcc cca aca cag cac acg gaa gct ttc    960
109 Ala Tyr Ala Pro Thr Ser Cys Ser Pro Thr Gln His Thr Glu Ala Phe
110 305                 310                 315                 320
112 gtg gtc ttc tac ttc cct ctc acc cac tgt gga acc aca atg cag gtg   1008
113 Val Val Phe Tyr Phe Pro Leu Thr His Cys Gly Thr Thr Met Gln Val
114                 325                 330                 335
116 gct ggc gac cag ctc atc tat gag aac tgg ctg gtg tct ggc atc cac   1056
117 Ala Gly Asp Gln Leu Ile Tyr Glu Asn Trp Leu Val Ser Gly Ile His
118             340                 345                 350
120 atc caa aag ggg cca cag ggt tcc atc acg cgg gac agc acc ttc cag   1104
121 Ile Gln Lys Gly Pro Gln Gly Ser Ile Thr Arg Asp Ser Thr Phe Gln
122             355                 360                 365
124 ctt cat gtg cgc tgt gtc ttc aac gcc agt gac ttc ctg ccc att cag   1152
125 Leu His Val Arg Cys Val Phe Asn Ala Ser Asp Phe Leu Pro Ile Gln
126         370                 375                 380
129 gca tcc att ttc cca ccc cca tcg cct gct cct atg acc cag ccc ggc   1200
130 Ala Ser Ile Phe Pro Pro Pro Ser Pro Ala Pro Met Thr Gln Pro Gly
131 385                 390                 395                 400
133 ccc ctg cgg ctt gag ctg cgg att gcc aaa gac gag acc tgc agc tcg   1248
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134 Pro Leu Arg Leu Glu Leu Arg Ile Ala Lys Asp Glu Thr Cys Ser Ser
135             405                 410                 415
137 tac tat ggg gag gat gac tat ccc atc gtg agg ctg ctc cga gaa cca    1296
138 Tyr Tyr Gly Glu Asp Asp Tyr Pro Ile Val Arg Leu Leu Arg Glu Pro
139             420                 425                 430
141 gtc cat gtg gag gtc cgg ctt ctg cag agg aca gac ccc aac ctg gtc    1344
142 Val His Val Glu Val Arg Leu Leu Gln Arg Thr Asp Pro Asn Leu Val
143             435                 440                 445
145 ctg ctg ctg cac cag tgc tgg ggc gct ccc agt gcc aac ccc ttc cag    1392
146 Leu Leu Leu His Gln Cys Trp Gly Ala Pro Ser Ala Asn Pro Phe Gln
147         450                 455                 460
149 cag ccc cag tgg ccc atc ctg tca gac ggc tgc cct ttc aag ggc gac    1440
150 Gln Pro Gln Trp Pro Ile Leu Ser Asp Gly Cys Pro Phe Lys Gly Asp
151 465                 470                 475                 480
153 agc tac aga acc caa atg gta gcc ttg gac ggg gcc aca cct ttc cag    1488
154 Ser Tyr Arg Thr Gln Met Val Ala Leu Asp Gly Ala Thr Pro Phe Gln
155             485                 490                 495
157 tcg cac tac cag cga ttc act gtt gct acc ttc gcc ctc ctg gac tca    1536
158 Ser His Tyr Gln Arg Phe Thr Val Ala Thr Phe Ala Leu Leu Asp Ser
159             500                 505                 510
161 ggc tcc cag aga gcc ctc aga gga ctg gtt tac ttg ttc tgc agc acc    1584
162 Gly Ser Gln Arg Ala Leu Arg Gly Leu Val Tyr Leu Phe Cys Ser Thr
163             515                 520                 525
165 tct gcc tgc cac acc tca ggg ctg gag act tgc tcc act gca tgt agc    1632
166 Ser Ala Cys His Thr Ser Gly Leu Glu Thr Cys Ser Thr Ala Cys Ser
167         530                 535                 540
169 act ggc act aca aga cag cga cga tcc tca ggt cac cgt aat gac act    1680
170 Thr Gly Thr Thr Arg Gln Arg Arg Ser Ser Gly His Arg Asn Asp Thr
171 545                 550                 555                 560
173 gcc agg ccc cag gac atc gtg agc tct ccg ggg cca gtg ggc ttt gag    1728
174 Ala Arg Pro Gln Asp Ile Val Ser Ser Pro Gly Pro Val Gly Phe Glu
175             565                 570                 575
177 gat tct tat ggg cag gag ccc aca ctt ggg ccc aca gac tcc aat ggg    1776
178 Asp Ser Tyr Gly Gln Glu Pro Thr Leu Gly Pro Thr Asp Ser Asn Gly
179             580                 585                 590
181 aac tcc agc ctg aga cct ctc ctt tgg gcg gtc ctt ttg ctg cca gct    1824
182 Asn Ser Ser Leu Arg Pro Leu Leu Trp Ala Val Leu Leu Leu Pro Ala
183         595                 600                 605
185 gtt gcc ctg gtc ctt ggg ttt ggt gtc ttt gtg ggc ctg agc cag acc    1872
186 Val Ala Leu Val Leu Gly Phe Gly Val Phe Val Gly Leu Ser Gln Thr
187         610                 615                 620
189 tgg gcc cag aag ctc tgg gaa agc aac aga cag tga                     1908
190 Trp Ala Gln Lys Leu Trp Glu Ser Asn Arg Gln  *
191 625                 630                 635
194 <210> SEQ ID NO: 2
195 <211> LENGTH: 635
196 <212> TYPE: PRT
197 <213> ORGANISM: Homo sapiens
199 <400> SEQUENCE: 2
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200 Met Ala Gly Gly Ser Ala Thr Thr Trp Gly Tyr Pro Val Ala Leu Leu
201 1               5               10              15
202 Leu Leu Val Ala Thr Leu Gly Leu Gly Arg Trp Leu Gln Pro Asp Pro
203             20              25              30
204 Gly Leu Arg His Ser Tyr Asp Cys Gly Ile Lys Gly Met Gln Leu Leu
205         35              40              45
206 Val Phe Pro Arg Pro Gly Gln Thr Leu Arg Phe Lys Val Val Asp Glu
207 .   50              55              60
208 Phe Gly Asn Arg Phe Asp Val Asn Asn Cys Ser Ile Cys Tyr His Trp
209 65              70              75              80
210 Val Thr Ser Arg Pro Gln Glu Pro Ala Val Phe Ser Ala Asp Tyr Arg
211             85              90              95
212 Gly Cys His Val Leu Glu Lys Asp Gly Arg Phe His Leu Arg Val Phe
213         100             105             110
215 Met Glu Ala Val Leu Pro Asn Gly Arg Val Asp Val Ala Gln Asp Ala
216     115             120             125
217 Thr Leu Ile Cys Pro Lys Pro Asp Pro Ser Arg Thr Leu Asp Ser Gln
218     130             135             140
219 Leu Ala Pro Pro Ala Met Phe Ser Val Ser Thr Pro Gln Thr Leu Ser
220 145             150             155             160
221 Phe Leu Pro Thr Ser Gly His Thr Ser Gln Gly Ser Gly His Ala Phe
222             165             170             175
223 Pro Ser Pro Leu Asp Pro Gly His Ser Ser Val His Pro Thr Pro Ala
224             180             185             190
225 Leu Pro Ser Pro Gly Pro Gly Pro Thr Leu Ala Thr Leu Ala Gln Pro
226         195             200             205
227 His Trp Gly Thr Leu Glu His Trp Asp Val Asn Lys Arg Asp Tyr Ile
228 .   210             215             220
229 Gly Thr His Leu Ser Gln Glu Gln Cys Gln Val Ala Ser Gly His Leu
230 225             230             235             240
231 Pro Cys Ile Val Arg Arg Thr Ser Lys Glu Ala Cys Gln Gln Ala Gly
232             245             250             255
233 Cys Cys Tyr Asp Asn Thr Arg Glu Val Pro Cys Tyr Tyr Gly Asn Thr
234         260             265             270
235 Ala Thr Val Gln Cys Phe Arg Asp Gly Tyr Phe Val Leu Val Val Ser
236     275             280             285
237 Gln Glu Met Ala Leu Thr His Arg Ile Thr Leu Ala Asn Ile His Leu
238     290             295             300
239 Ala Tyr Ala Pro Thr Ser Cys Ser Pro Thr Gln His Thr Glu Ala Phe
240 305             310             315             320
241 Val Val Phe Tyr Phe Pro Leu Thr His Cys Gly Thr Thr Met Gln Val
242             325             330             335
243 Ala Gly Asp Gln Leu Ile Tyr Glu Asn Trp Leu Val Ser Gly Ile His
244         340             345             350
245 Ile Gln Lys Gly Pro Gln Gly Ser Ile Thr Arg Asp Ser Thr Phe Gln
246         355             360             365
247 Leu His Val Arg Cys Val Phe Asn Ala Ser Asp Phe Leu Pro Ile Gln
248     370             375             380
249 Ala Ser Ile Phe Pro Pro Pro Ser Pro Ala Pro Met Thr Gln Pro Gly
```

```
                    RAW SEQUENCE LISTING                    DATE: 08/13/2001
                    PATENT APPLICATION:  US/09/922,488      TIME: 11:25:00

                    Input Set : A:\0054.txt
                    Output Set: N:\CRF3\08132001\I922488.raw

250 385                     390                   395                   400
251 Pro Leu Arg Leu Glu Leu Arg Ile Ala Lys Asp Glu Thr Cys Ser Ser
252                         405                   410                   415
253 Tyr Tyr Gly Glu Asp Asp Tyr Pro Ile Val Arg Leu Leu Arg Glu Pro
254                         420                   425                   430
255 Val His Val Glu Val Arg Leu Leu Gln Arg Thr Asp Pro Asn Leu Val
256             435                   440                   445
258 Leu Leu Leu His Gln Cys Trp Gly Ala Pro Ser Ala Asn Pro Phe Gln
259         450                       455                   460
260 Gln Pro Gln Trp Pro Ile Leu Ser Asp Gly Cys Pro Phe Lys Gly Asp
261 465                         470                   475                   480
262 Ser Tyr Arg Thr Gln Met Val Ala Leu Asp Gly Ala Thr Pro Phe Gln
263                         485                   490                   495
264 Ser His Tyr Gln Arg Phe Thr Val Ala Thr Phe Ala Leu Leu Asp Ser
265             500                   505                   510
266 Gly Ser Gln Arg Ala Leu Arg Gly Leu Val Tyr Leu Phe Cys Ser Thr
267             515                   520                   525
268 Ser Ala Cys His Thr Ser Gly Leu Glu Thr Cys Ser Thr Ala Cys Ser
269     530                       535                   540
270 Thr Gly Thr Thr Arg Gln Arg Arg Ser Ser Gly His Arg Asn Asp Thr
271 545                         550                   555                   560
272 Ala Arg Pro Gln Asp Ile Val Ser Ser Pro Gly Pro Val Gly Phe Glu
273                         565                   570                   575
274 Asp Ser Tyr Gly Gln Glu Pro Thr Leu Gly Pro Thr Asp Ser Asn Gly
275             580                   585                   590
276 Asn Ser Ser Leu Arg Pro Leu Leu Trp Ala Val Leu Leu Leu Pro Ala
277         595                   600                   605
278 Val Ala Leu Val Leu Gly Phe Gly Val Phe Val Gly Leu Ser Gln Thr
279     610                   615                   620
280 Trp Ala Gln Lys Leu Trp Glu Ser Asn Arg Gln
281 625                     630                   635
284 <210> SEQ ID NO: 3
285 <211> LENGTH: 1905
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: degenerate nucleotide sequence
292 <221> NAME/KEY: misc_feature
293 <222> LOCATION: 6, 9, 12, 15, 18, 21, 24, 30, 36, 39, 42, 45, 48, 51, 54,
294         57, 60, 63, 66, 69, 72, 75, 78, 84, 90, 96, 99, 102, 105,
295         111, 123, 132, 141, 144, 147, 153, 156, 159, 162, 168, 171,
296         174, 183, 186, 198, 204, 213, 225, 243, 246, 249, 252
297 <223> OTHER INFORMATION: n = A,T,C or G
299 <221> NAME/KEY: misc_feature
300 <222> LOCATION: 255, 264, 267, 270, 276, 279, 288, 291, 300, 303, 315, 318,
301         327, 330, 333, 345, 348, 351, 354, 360, 363, 366, 372, 375,
302         384, 387, 390, 399, 405, 411, 414, 417, 420, 423, 429, 435,
303         438, 441, 444, 447, 456, 459, 462, 465, 468, 474, 477
304 <223> OTHER INFORMATION: n = A,T,C or G
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 08/13/2001
PATENT APPLICATION: US/09/922,488   TIME: 11:25:01

Input Set : **A:\0054.txt**
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```
L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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